TRENCE 1 (Graves 1 to 7542)

BRANCE (TIME AND THE TOTAL TO THE TOTAL T linear ROD 24-OCT-1998 T-type calcium channel 7542 bp mRNA voltage-activated, T-3) mRNA, complete cds. 6856 ACCCAACAGACATGGACCCC 6875 egicus low va jt (CACNAIG) SPMetAspPro N Rattus norve 84503 Subani N AF027984 AF027984 1 2280 sperothra DEFINITION ACCESSION VERSTON KEYWORDS SOURCE ORGANISM Bource REFERENCE AUTHORS JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL RNCAA1G LOCUS REMARK COMMENT PEATURES gene TITLE

VVLMKTMDNVATFCMLLMLF1F1FS1LGMHLFGCKFASERDGDTLPDRKNFDSLLWAI
VVLMKTMDNVATFCMLLMLF1F1FS1LGMHLFGCKFASERDGDTLPDRKNFDSLLWAI
VTVFQ1LTQEDWNKVLXNGMASTSSWAALYF1ALMTFGNYVLFNLLVAILVEGFQAEG
SSSTGVGEALGSGSRRTSLSGEGAEPGAAHTEMKCPPSARSSPHSPWSAASSWTSRRS
RNSLGRAPSLKRRSPSGERRSLLSGEGGESQDEEESSEBDRASPAGSBHRRGSLERE
BAGSTLANGERTONDSCRSASEDOGESSBEDRASPAGSBHRRGSLERE
DEGNISKGERTIOAWYRSTLDPRGASTIFLTLCHRIITHMPDQLGDDDN
VIIFLNCITIAMERPRIDAMARSILPACKERDSWAYIFFOORFLCHRIITHMPDVVL
LRSSWNVLDGLLVLISVIDILVSWYSBSGTKILGMLRVLRLLCHRIITHMPDHVVVL
LRSSWNVLDGLLVLISVIDILVSWYSBSGTKILGMLRVLRLLRTLRPLRVISRAQGLK
ASYRWVRHKYNFDNLGOALMSLFVLASKDGWVDINYDGLDAVGVOOPDIMHNPWMLL
MAEAQCKRYYSDYSRFRLLVHHLCTSHYLDLFITGVGGNVVTWAMEHYQQPQILLDEA
LVICNYIFTVIFVESVKVLANFFKCRQHQEEEBRRREEKRLRRLEKKRRSKEKQ
LKICNYIFTVIFVESVYKADYAFGFRRFFQDRWNQLDLAIVLLSIMGITLEFIFA
AGSTCYNTVISPIYFVGAFGRRFFQDRWNQLDLAIVLLSIMGITLEFIFA
QESTCYNTVISPIYFVGSVKLLYAAFGFRRFFQDRWNQLDLAIVLLSIMGITLEFIFA
ALGVELFGDLECDETHPCEGLGRHATFRNFGMAFLLTFRVSTGDNWNGIMKDTLRDCD
MKTLSPQPHSPLGSPFLWPGVGVNSTDSPKRGAPHTTAHIGAASGFSLEHPTWVPHP
SVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPRFRGKREAKEREAELEBE
EEVPVDLGFDLLTVRKSGVSRTHSLPNDSYMCRNGSTARRSLGHRGWGLPRAPRP
CPGLEPRWAKDPPETRSSLELDTELSHISGDLLPSSQEEPLFPRDLKKCYSVFTQSCR
DPPESQGSRPPCSPGVCLRRRAPASDSKCDPSVSSPLGGPGSPPFRRDLKCYSVFTGSCR
DPPESQGSRPPCSPGVCLRRRAPASDSKCDPSVSSPLDSTAASPSPKKDTLSLSG

0 10 10 Length:
Matches:
Conservative:
Mismatches:
Indels: (1-7542)US-09-611-257A-24 (1-2287) x RNCAAIG 99.78% Percent Similarity: Best Local Similarity; Query Match: Alignment Scores: Pred. No.: . No.: Score:

444 1 MetLeuProHisArgValProArgCysValArgThrProProLeuArgGlySerAlaArg ProSerSerAspProProGlyProArgLeuAlaArgGlyTrpThrArgArgArgMetGlu 21 g ò

41 ArgalaproargSerArgAspSerProvalAlaSerArgSerSerThrThrCysProGly 505 61 8 g ò

445

a

504

40

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100 624

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80 laGluGlyLeuProTyrProAlaLeuAlaProValValPhePheTyrLeuSerGlnAspS 셤 ð g

etLeuValIleLeuLeuAsnCysValThrLeuGlyMetPheArgProCysGluAspIleA 120 g ò g 8

100

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160 864 heAlaValGluMetValValLySMetValAlaLeuGlyIlePheGlyLySLySCysTyrL 160 엄

ORIGIN

8

Oy 540 lyAsnGlyThrLeuArgValProArgAlaSerProGluIleGlnAspArgAspAlaAsnG	Qy 600 ysGlnAlaProProProArgCysProSerGluAlaSerGlyArgThrValGlySerGlyL Db 2185 GCCAGGCACCCCTCCCAGATGCCCATCGGAGGCATCTGGTAGGACTGTGGGAAGTGGGAA Qy 620 ysValTyrProThrValHisThrSerProProProGluIleLeuLysAspLysAlaLeuV Db 2245 AGGTGTACCCCACTGTGCATACCAGCCTCCACAGAGATAAAGCACTAG	230	DD 2365 CCITCAGCICCAIGCACAAGCICCTGGAGACACAGAGIACGGAGGCCTGCCAIAGCT Qy 680 ysLyslleSerSerProCysSerLysAlaAspSerGlyAlaCysGlyProAspSerC	00 85	720	Oy 740 rohisSerArgArgArgGlnArgSerLeuGlyProAspAlaGluProSerSerValLeuA	Qy 760 laPheTrpArgLeuileCysAspThrPheArgLysileValAspSerLysTyrPheGlyA	Oy 780 rgGly11eMet11eAlaIleLeuValAsnThrLeuSerMetGly11eGluTyrHisGluG	800 InProGluGluLeuThrAsnAlaLeuGluIleSerAsnIleValPheThrSerLeu 	Oy 820 laLeuGluMetLeuLeuLysLeuLeuValTyrGlyProPheGlyTyrIleLysAsnProT	840 yrA 2905 ACA	Qy 860 lyGlyLeuSerValLeuArgThrPheArgLeuMetArgValLeuLysLeuValA	3025
180 euGlyAspThrTrpAsnArgLeuAspPhePheIleValIleAlaGlyMetLeuGluTyrS 200 [euPrometLeuGlyAsnValLeuLeuLeuCysPhePheValPhePheIlePheGlyIleV	1185 TGGGCGTCCAGCTGTGGGGGGGTTCCTCCCCCGAGAACTTCA 1224 280 erLeuProLeuSerValAspLeuGluProTyrTyrGlnThrGluAsnGluAspGluSerP 300	ccrrcatcrgcrcrcagccrcagagaargccaraagarccrgcagagrgraccacac 13 euargglygluglyglyglyglyProProCysSerLeuaspTyrGluThrTyrasnSerS 34	1345 TGCGTGGGGTGGCGTGGCCCACCCTGCAGTCTGGACTATGAGACCTATAACAGTT 1404 340 erSerAsnThrThrCysValAsnTrpAsnGlnTyrTyrThrAsnCysSerAlaGlyGluH 360	isAsnProPheLysGlyAlaIleAsnPheAspAsnIleGlyTyrAlaTrpIleAlaIleP 38 	380 heGlnValIleThrLeuGluGlyTrpValAspIleMetTyrPheValMetAspAlaHisS 400	400 erPheTyrAsnPheIleTyrPheIleLeuLeuIleIleValGlySerPhePheMetIleA 420	∞ —≪	0—H	460 luProGlySerCysTyrGluGluLeuLeuLysTyrLeuValTyrIleLeuArgLysAlaA 480 		roValAlaArgSerGlyGlnGluProGlnProSerGlySerCysThrArgSerHisArgA 5	520 rgLeuServalHisHisLeuValHisHisHisHisHisHisHisHisHisHisHisTyrHisLeuG 5

65 GAGAGCGAGATTC	80 80 7 80 80 80	00 snCyslleThr1 	1320 heleuThrleuSerAsnTyr] 	1340 alvalAlaLeuGlyTrpCysI 	1360 euAspGlyLeuLeuValLeu 	1380 erGlyThrLysIleLeuGlyt 	585	420 645	440 e 705 T	0 20	80 heAs 25 TTGA	o alaspilemetrylaspor	1	9 - C 0 - C 1 - C	9 2 0	25 G—e	85 T	1620 alileGlyLeuAsnValVal7
qa —		. qa	- G	oy Ob	\$ 8 -	\$ 6 6	ý d	& 43 	`& £	ò 8	ò 8 5	÷ € €	÷ 6 €	ò a	ò a .	충 옵 _. 8	· 옵	ර සි
3085 CCTTCTGCATGCTCCTCATCTTCATCTTCAGCATCCTGGGCATGCAT	920 heGlyCyBLyBPheAlaSerGluArgABpGlyABpThrLeuProABpArgLyBABnPheA 940 	940 spSerLeuLeuTrpAlaIleValThrValPheGlnIleLeuThrGlnGluAspTrpAsnL 960 	960 ysValLeuTyrAsnGlyMetAlaSerThrSerSerTrpAlaAlaLeuTyrPheileAlaL 980	265 AAGTCCTCTACAACGCCTGGCCTCCACATCGTCTTGGGCTGCTCTTTACTTCATCGCCC 332. 980 euMetThrPheGlyAsnTyrValLeuPheAsnLeuLeuValAlaIleLeuValGluGlyP 100.	325 TCATGACTTTTGGCAACTATGTGCTCTTTAACCTGCTGGTGGCCATTCTTGTGGAAGGAL 338 000 heGlnAlaGluGlyAspAlaThrLysSerGluSerGluProAspPhePheSerProSerV 102 	385 TCCAGGCAGAGGGAGATGCCACCAAGTCTGAGTC 020 alAspGlyAspGlyAspArgLysLysArgLeuAl	etisthralaalathrPrometSert 106	060 isProLysSerSerSerThrGlyValGlyGluAl 	080 erSerSerGlySerAlaGluProGlyAlaAlaHi 	0 laargSerSerProHisSerProTrpSerAlaal 	0 erArgAenSerLeuGlyArgAlaProSerLeuL 	1140 rgSerLeuLeuSerGlyGluGlyGlnGluSerGlnAspGluGluGluSerSerGluGluA 1160 	1160 spargalaSerProalaGlySerAspHisArgHisArgGlySerLeuGluArgGluAlaL 1180 	180	200 lyArgSerSeralaSerGluHisGlnAspCysAsnGlyLysSerAlaSerGlyArgLeuA 12:	1220 laargThrLeuargThrAspAspProGlnLeuAspGlyAspAspAspAspAspAspGluGlyA 1240 	1240 snLeuSerLysGlyGluArglleGlnAlaTrpValArgSerArgLeuProAlaCysCysA 12 	1260 rgGluArgAspSerTrpSerAlaTyrIlePheProProGlnSerArgPheArgLeuLeuC 1280
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1500 4704 1460 1480 4824 4884 1.valvalgluasnPheHisLysCysArgGlnHisGlnGluG 3GCCTATATCTTTCCTCCTCAGGTTTCGTCTCCTGT

00 erCyslleLeuGlnLeuProLysAspValHisTyrLeuLeuGlnProHisGlyAlaProT 20	Oy 2060 luAspLeuLeuSerGluValSerGlyProSerCysProLeuThrArgSerSerPheT 2080	Oy 2100 isIleArgLeuProAlaProCysProGlyLeuGluProSerTrpAlaLysAspProProG 2120	216	6865 CCCAGAGCTGCAGGCCTGGGTTCTGGCTAGATGAACAGCGGAGACACTCCATTG 692. 2180 laValSerCY8LeuAspSerGlySerGlnProArgLeuCy8ProSerProSerSerLeuG 220 [2200 lyGlyGlnProLeuGlyGlyProGlySerArgProLyBLyBLyBLeuSerProProSerI 22	2220 leserileasprofrogluserginglyserargfrocysserproglyvalcysb 224	######################################	QY 2280 spProThraspMetAspPro 2286	channel.	SION BD224079.1 GI:3303384 WORDS JP 2002525077-A/2. RCE Rattus sp.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1640 spGluAlaLeuLysIleCysAsnTyrIlePheThrValilePheValPheGluSerValP 1660	1700 erLeuProlleAsnProThrileIleArgileMetArgValLeuArgileAlaArgValL 1720	0 euProGlnValGlyAsnLeuGlyLeuLeuPheMetLeuLeuPhePheIlePheAlaAlaL 176	5 7 5	1800 hrGlyAspAsnTrpAsnGlyIleMetLysAspProSerArgAspCysAspGlnGluserT 1820	0 heValLeuValAsnValValIleAlaValLeuMetLySHisLeuGluGluSerAsnLySG 186 	1860 luAlaLysGluGluAlaGluLeuGluAlaGluLeuGluMetLysThrLeuSerP 1880	6025 CGCAGCCCCACTCCCCGCTGGGCAGCCCCTTCCTTGGCCCGGGGTGGAGGGTCAACA 6084 1900 erThrAspSerProLysProGlyAlaProHisThrThrAlaHisIleGlyAlaAlaSerG 1920 1910	0 lyPheSerLeuGluHisProThrMetValProHisProGluGluValProValProLeuG 194	0 lyProAspLeuLeuThrValArgLysSerGlyValSerArgThrHisSerLeuProAsnA 196 	1960 spSerTyrMetCysArgAsnGlySerThrAlaGluArgSerLeuGlyHisArgGlyTrpG 1980 	1980 lyLeuProLysAlaGlnSerGlySerIleLeuSerValHisSerGlnProAlaAspThrS 2000